

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 1999, 22:34:36 ; Search time 360.53 seconds  
(without alignments)  
38.080 Million cell updates/sec

Title: US-09-205-015-1  
Perfect score: 9  
Sequence: 1 tctgagtca 9

Scoring table: IDENTITY\_NUC

Searched: 2002476 seqs, 762712212 residues

Database : EST.\*  
1: em\_est1:\*  
2: em\_est2:\*  
3: em\_est3:\*  
4: em\_est4:\*  
5: em\_est5:\*  
6: em\_est6:\*  
7: em\_est7:\*  
8: em\_est8:\*  
9: em\_est9:\*  
10: gb\_est1:\*  
11: gb\_est2:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: gb\_est6:\*  
16: gb\_est7:\*  
17: gb\_est8:\*  
18: gb\_est9:\*  
19: gb\_est10:\*  
20: gb\_est11:\*  
21: gb\_est12:\*  
22: gb\_est13:\*  
23: gb\_est22:\*  
24: gb\_est14:\*  
25: gb\_est15:\*  
26: gb\_est16:\*  
27: gb\_est17:\*  
28: gb\_est18:\*  
29: gb\_est19:\*  
30: gb\_est20:\*  
31: gb\_est21:\*  
32: em\_est10:\*  
33: em\_est11:\*  
34: em\_est12:\*  
35: em\_est13:\*  
36: em\_est14:\*  
37: em\_est15:\*  
38: em\_est16:\*  
39: em\_est17:\*  
40: em\_est18:\*  
41: em\_est19:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	9 100.0	986 10	HSU19036	U19036 Human chrom
c 2	9 100.0	408 10	M75753	M75753 CEL01A5 Cae

3	9	100.0	542	10	M75778	M75778 CEL02B10 Cae
4	9	100.0	490	10	M75815	M75815 CEL04C3 Cae
c 5	9	100.0	330	10	M79503	M79503 WEST00040 C
c 6	9	100.0	411	10	M89881	M89881 CEL12F7 Cae
c 7	9	100.0	451	10	M89247	M89247 CEL20B1 Cae
c 8	9	100.0	356	10	M89388	M89388 CEL22E8 Cae
c 9	9	100.0	434	10	MUSF231A	L26751 Mus musculus
c 10	9	100.0	436	10	MUSF259A	L26751 Mus musculus
c 11	9	100.0	496	10	R00048	R00048 ye70e03.s1
c 12	9	100.0	363	10	R00424	R00424 ye71h05.r1
c 13	9	100.0	411	10	R01268	R01268 ye81g05.s1
c 14	9	100.0	397	10	R01396	R01396 ye77a11.s1
c 15	9	100.0	379	10	R01864	R01864 ye84d12.s1
c 16	9	100.0	362	10	R02001	R02001 ye82b09.s1
c 17	9	100.0	422	10	R02139	R02139 ye87a01.s1
c 18	9	100.0	350	10	R03267	R03267 pk05e04.s1
c 19	9	100.0	376	10	R04520	R04520 pk24g01.s1
c 20	9	100.0	389	10	R05588	R05588 ye92a02.r1
c 21	9	100.0	278	10	R05679	R05679 yf12b05.r1
c 22	9	100.0	501	10	R06930	R06930 yf12b05.r1
c 23	9	100.0	440	10	R07369	R07369 ye96h06.s1
c 24	9	100.0	298	10	R08467	R08467 ye95b01.r1
c 25	9	100.0	428	10	R08746	R08746 yf20a11.s1
c 26	9	100.0	384	10	R08764	R08764 yf20d10.s1
c 27	9	100.0	241	10	R08849	R08849 yf21b08.s1
c 28	9	100.0	369	10	R09135	R09135 yf25f10.r1
c 29	9	100.0	421	10	R09518	R09518 yf27a04.s1
c 30	9	100.0	389	10	R09829	R09829 yf30a09.r1
c 31	9	100.0	466	10	R10075	R10075 yf35b02.s1
c 32	9	100.0	351	10	R10086	R10086 yf35c07.s1
c 33	9	100.0	337	10	R10246	R10246 yf32e07.r1
c 34	9	100.0	444	10	R10424	R10424 yf28f09.r1
c 35	9	100.0	403	10	R11110	R11110 yf39f01.r1
c 36	9	100.0	294	10	R11613	R11613 yf47e11.r1
c 37	9	100.0	457	10	R11682	R11682 yf49a07.r1
c 38	9	100.0	371	10	R12038	R12038 yf53e09.r1
c 39	9	100.0	391	10	R12308	R12308 yf55b02.r1
c 40	9	100.0	368	10	R12822	R12822 yf57c11.r1
c 41	9	100.0	407	10	R13319	R13319 yf75f03.r1
c 42	9	100.0	455	10	R13924	R13924 yf62f05.r1
c 43	9	100.0	404	10	R14091	R14091 yf69a08.r1
c 44	9	100.0	447	10	R14267	R14267 yf79e05.r1
c 45	9	100.0	587	31	C98064	C98064 Oryza sativ

ALIGNMENTS

RESULT 1

HSU19036 986 bp mRNA EST 09-MAR-1995  
LOCUS Human chromosome 5q12 clone XS2G3 mRNA, 3'UTR.  
DEFINITION  
ACCESSION U19036  
NID 9643632  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 980)

Thompson,T.G., DiDonato,C.J., Simard,L.R., Ingram,S.E., Burghes,A.H.-M., Crawford,T.O., Rochette,C., Mendell,J.R. and Wasmuth,J.J.

A novel cDNA detects homozygous microdeletions in greater than 50% of type I spinal muscular atrophy patients Nature Genet. 9, 56-62 (1995)

Thompson,T.G.

Direct Submission

TITLE

JOURNAL

REFERENCE

AUTHORS

COMMENT

```

FEATURES          Location/Qualifiers
  source          1..986
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone="XS2G3"
                  /chromosome="5"
                  /map="5q12"
polyA_site        986
BASE COUNT        325 a 177 c 192 g 292 t
ORIGIN
Query Match      100.0%; Score 9; DB 10; Length 986;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctgagtca 9
|||||
Db 170 TCTGAGTCA 178

RESULT 2
M75753/c          408 bp mRNA EST 16-SEP-1992
LOCUS             M75753
DEFINITION        CELO1A5 Caenorhabditis elegans cDNA clone cm01a5 5'.
ACCESSION         M75753
NID               9275030
KEYWORDS          EST.
SOURCE            Nematodes clone-cm01a5 library-Chris Martin sorted cDNA library
                  strain-Bristol N2 vector-lambda phage SHLX2 host-MC1061 Mixed stage
                  hermaphrodite cDNA library. Partially normalized by successively
                  picking groups of clones that didn't hybridize to previously picked
                  clones. Vector: lambda phage SHLX2 (Lipshitz, D.H. et al., Gene
                  88:25-36 (1990)). Host: MC1061.
ORIGIN            Caenorhabditis elegans
Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae.
1 (bases 1 to 408)
Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A.,
Hillier,L., Durbin,R.K., Green,P., Shownkeen,R., Halloran,N.,
Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J.
and Sulston,J.
A survey of expressed genes in Caenorhabditis elegans
Nature Genet. 1, 114-123 (1992)
Contact: Waterston R.H.(USA) and Sulston J.E.(UK)
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Fax: (USA) (314)3624137 or (UK) (0223)402008
Email: rwenematode.wustl.edu or jes@mrc-lmb.cam.ac.uk.
FEATURES          Location/Qualifiers
  source          1..542
                  /organism="Caenorhabditis elegans"
                  /clone="cm02b10"
                  /strain="Bristol N2"
BASE COUNT        160 a 100 c 145 g 128 t 9 others
ORIGIN
Query Match      100.0%; Score 9; DB 10; Length 542;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctgagtca 9
|||||
Db 88 TCTGAGTCA 96

RESULT 4
M75815            490 bp mRNA EST 16-SEP-1992
LOCUS             M75815
DEFINITION        CELO4C3 Caenorhabditis elegans cDNA clone cm04c3 5'.
ACCESSION         M75815
NID               9275168
KEYWORDS          EST.
SOURCE            Nematodes clone-cm04c3 library-Chris Martin sorted cDNA library
                  strain-Bristol N2 vector-lambda phage SHLX2 host-MC1061 Mixed stage
                  hermaphrodite cDNA library. Partially normalized by successively
                  picking groups of clones that didn't hybridize to previously picked
                  clones. Vector: lambda phage SHLX2 (Lipshitz, D.H. et al., Gene
                  88:25-36 (1990)). Host: MC1061.
ORIGIN            Caenorhabditis elegans
Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae.
1 (bases 1 to 490)
Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A.,
Hillier,L., Durbin,R.K., Green,P., Shownkeen,R., Halloran,N.,
Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J.
and Sulston,J.
A survey of expressed genes in Caenorhabditis elegans
Nature Genet. 1, 114-123 (1992)
Contact: Waterston R.H.(USA) and Sulston J.E.(UK)
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Email: rwenematode.wustl.edu or jes@mrc-lmb.cam.ac.uk.
FEATURES          Location/Qualifiers
  source          1..408
                  /organism="Caenorhabditis elegans"
                  /clone="cm01a5"
                  /strain="Bristol N2"
BASE COUNT        115 a 89 c 97 g 102 t 5 others
ORIGIN
Query Match      100.0%; Score 9; DB 10; Length 408;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctgagtca 9
|||||
Db 144 TCTGAGTCA 136

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JOURNAL      Nature Genet. 1, 114-123 (1992)
COMMENT

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Fax: (USA) (314)3624137 or (UK) (0223)402008
Email: rw@nematode.wustl.edu or jes@mrc-lmb.cam.ac.uk.

FEATURES
source
1..490
/organism="Caenorhabditis elegans"
/clone="cm04c3"
/strain="Bristol N2"
BASE COUNT 135 a 100 c 111 g 141 t 3 others
ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 490;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
|||||
Db 61 TCTGAGTCA 69

RESULT 5
M79503/c
LOCUS M79503 330 bp mRNA EST 30-JUN-1992
DEFINITION WEST00040 Caenorhabditis elegans cDNA clone CEMSA23 similar to
Tropomyosin.
ACCESSION M79503
NID 9271528
KEYWORDS EST.
SOURCE
Nematodes clone-CEMSA23 library-Mixed reverse, Stratagene (cat.
#937006) vector-Uni-ZAP XR primer-M13 Reverse C. elegans mixed
stage cDNA library. Stratagene catalog #937006. The library is
oligo dT primed and directionally cloned in the Uni-ZAP XR vector.
ORGANISM Caenorhabditis elegans
Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae.
REFERENCE
1 (bases 1 to 330)
AUTHORS McCombie,W.R., Adams,M.D., Kelley,J.M., FitzGerald,M.G.,
Utterback,T.R., Khan,M., Dubnick,M., Kerlavage,A.R., Venter,J. and
Fields,C.
TITLE Caenorhabditis elegans expressed sequence tags reveal gene families
and potential disease gene homologues
JOURNAL Nature Genet. 1, 124-131 (1992)
COMMENT *Other_ESTs: WEST00039
Contact: Kerlavage AR
The Institute for Genomic Research
932 Clopper Road,Gaithersburg,MD 20878
Tel: 3018690056
Fax: 301869423
Email: arkerl@vetigr.org.
FEATURES
source
1..330
/organism="Caenorhabditis elegans"
/clone="CEMSA23"
BASE COUNT 100 a 74 c 88 g 52 t 6 others
ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 330;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
|||||
Db 188 TCTGAGTCA 180

JOURNAL      Nature Genet. 1, 114-123 (1992)
COMMENT

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Email: rw@nematode.wustl.edu or jes@mrc-lmb.cam.ac.uk.

FEATURES
source
1..490
/organism="Caenorhabditis elegans"
/clone="cm04c3"
/strain="Bristol N2"
BASE COUNT 135 a 100 c 111 g 141 t 3 others
ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 490;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
|||||
Db 61 TCTGAGTCA 69

RESULT 5
M79503/c
LOCUS M79503 330 bp mRNA EST 30-JUN-1992
DEFINITION WEST00040 Caenorhabditis elegans cDNA clone CEMSA23 similar to
Tropomyosin.
ACCESSION M79503
NID 9271528
KEYWORDS EST.
SOURCE
Nematodes clone-CEMSA23 library-Mixed reverse, Stratagene (cat.
#937006) vector-Uni-ZAP XR primer-M13 Reverse C. elegans mixed
stage cDNA library. Stratagene catalog #937006. The library is
oligo dT primed and directionally cloned in the Uni-ZAP XR vector.
ORGANISM Caenorhabditis elegans
Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae.
REFERENCE
1 (bases 1 to 330)
AUTHORS McCombie,W.R., Adams,M.D., Kelley,J.M., FitzGerald,M.G.,
Utterback,T.R., Khan,M., Dubnick,M., Kerlavage,A.R., Venter,J. and
Fields,C.
TITLE Caenorhabditis elegans expressed sequence tags reveal gene families
and potential disease gene homologues
JOURNAL Nature Genet. 1, 124-131 (1992)
COMMENT *Other_ESTs: WEST00039
Contact: Kerlavage AR
The Institute for Genomic Research
932 Clopper Road,Gaithersburg,MD 20878
Tel: 3018690056
Fax: 301869423
Email: arkerl@vetigr.org.
FEATURES
source
1..330
/organism="Caenorhabditis elegans"
/clone="CEMSA23"
BASE COUNT 100 a 74 c 88 g 52 t 6 others
ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 330;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
|||||
Db 188 TCTGAGTCA 180

JOURNAL      Nature Genet. 1, 114-123 (1992)
COMMENT

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FEATURES
source
1..411
/organism="Caenorhabditis elegans"
/clone="cm12f7"
/strain="Bristol N2"
BASE COUNT 120 a 85 c 97 g 105 t 4 others
ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 411;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
|||||
Db 121 TCTGAGTCA 113

RESULT 7
M89247/c
LOCUS M89247 461 bp mRNA EST 02-DEC-1992
DEFINITION CEL20B1 Caenorhabditis elegans cDNA clone cm20b1 5' similar to
Ca2+-transporting ATPase homologous peptide.
ACCESSION M89247
NID 9275748
KEYWORDS EST.
SOURCE
Nematodes clone-cm20b1 library=Chris Martin sorted cDNA library
strain-Bristol N2 vector-lambda phage SHLX2 host-MC1061 Mixed stage
hermaphrodite cDNA library. Partially normalized by successively
picking groups of clones that didn't hybridize to previously picked
clones. Vector: lambda phage SHLX2 (Lipshitz, D.H. et al., Gene
88:25-36 (1990)) Host: MC1061.
ORGANISM Caenorhabditis elegans
Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae.
REFERENCE
1 (bases 1 to 461)
AUTHORS Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A.,

```

Hillier,L., Durbin,R.K., Green,P., Shownkeen,R., Halloran,N.,  
Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J.,  
and Sulston,J.  
A survey of expressed genes in Caenorhabditis elegans  
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Fax: (USA) (314)3624137 or (UK) (0223)402008  
Email: rwenematode.wustl.edu or jes@rc-lmb.cam.ac.uk.

## FEATURES

source  
1. .461  
/organism="Caenorhabditis elegans"  
/clone="cm20b1"  
/strain="Bristol N2"

BASE COUNT 136 a 120 c 109 g 94 t 2 others  
ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 461;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9  
|||||

Db 67 TCTGAGTCA 59

## RESULT

M89388/c 356 bp mRNA EST 16-SEP-1992  
LOCUS CEL22E8 Caenorhabditis elegans cDNA clone cm22e8 5'  
DEFINITION M89388  
ACCESSION 9275893  
NID  
KEYWORDS  
SOURCE

Nematodes clone-cm22e8 library-Chris Martin sorted cDNA library  
strain-Bristol N2 vector-lambda phage SHLX2 host-MC1061 Mixed stage  
hermaphrodite cDNA library. Partially normalized by successively  
picking groups of clones that didn't hybridize to previously picked  
clones. Vector: lambda phage SHLX2 (Lipshitz, D.H. et al., Gene  
88:25-36 (1990)) Host: MC1061.

Caenorhabditis elegans  
Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida;  
Rhabditina; Rhabditoidea; Rhabditidae.

1 (bases 1 to 356)

Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A.,  
Hillier,L., Durbin,R.K., Green,P., Shownkeen,R., Halloran,N.,  
Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J.,  
and Sulston,J.  
A survey of expressed genes in Caenorhabditis elegans  
Nature Genet. 1, 114-123 (1992)

## TITLE

## JOURNAL

## COMMENT

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Fax: (USA) (314)3624137 or (UK) (0223)402008  
Email: rwenematode.wustl.edu or jes@rc-lmb.cam.ac.uk.

## FEATURES

source  
1. .356  
/organism="Caenorhabditis elegans"  
/clone="cm22e8"  
/strain="Bristol N2"

BASE COUNT 110 a 62 c 80 g 102 t 2 others  
ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 356;  
Best Local Similarity 100.0%; Pred. No. 6e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9  
|||||

Db 294 TCTGAGTCA 286

## RESULT

MUSF231A 434 bp mRNA EST 24-FEB-1995  
LOCUS Mus musculus expressed sequence tag EST F231, mRNA sequence.  
DEFINITION L26742  
ACCESSION 9437523  
NID  
KEYWORDS  
SOURCE

EST; expressed sequence tag.  
Mus musculus (strain Swiss) (tissue library: lambda unizap) male  
testis cDNA to mRNA.

ORGANISM  
Mus musculus  
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
Murinae; Mus.

1 (bases 1 to 434)

Kerr,S.M., Vambrie,S., McKay,S.J. and Cooke,H.J.  
Analysis of cDNA sequences from mouse testis  
Mamm. Genome 5 (9), 557-565 (1994)

FEATURES  
Location/Qualifiers

1. .434  
/organism="Mus musculus"  
/strain="Swiss"  
/db\_xref="taxon:10090"  
/sex="male"  
/tissue.type="testis"  
/tissue\_lib="lambda unizap"  
BASE COUNT 133 a 82 c 64 g 154 t 1 others  
ORIGIN

Query Match 100.0%; Score 9; DB 10; Length 434;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9  
|||||

Db 280 TCTGAGTCA 288

## RESULT

MUSF259A/c 436 bp mRNA EST 24-FEB-1995  
LOCUS Mus musculus expressed sequence tag EST F259, mRNA sequence.  
DEFINITION L26751  
ACCESSION 9437531  
NID  
KEYWORDS  
SOURCE

EST; expressed sequence tag.  
Mus musculus (strain Swiss) (tissue library: lambda unizap) male  
testis cDNA to mRNA.

ORGANISM  
Mus musculus  
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
Murinae; Mus.

1 (bases 1 to 436)

Kerr,S.M., Vambrie,S., McKay,S.J. and Cooke,H.J.  
Analysis of cDNA sequences from mouse testis  
Mamm. Genome 5 (9), 557-565 (1994)

FEATURES  
Location/Qualifiers

1. .436  
/organism="Mus musculus"  
/strain="Swiss"  
/db\_xref="taxon:10090"

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/sex="male"
/tissue_type="testis"
/tissue_lib="lambda unizap"
BASE COUNT      131 a   76 c  112 g  116 t      1 others
ORIGIN

Query Match      100.0%; Score 9; DB 10; Length 436;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9
|||||
Db 202 TCTGAGTCA 194

RESULT 11
R00048
LOCUS      496 bp      mRNA      EST      31-MAR-1995
DEFINITION ye70e03.s1 Homo sapiens cDNA clone 123100 3'.
ACCESSION  R00048
NID         9749784
KEYWORDS   EST.
SOURCE     human clone-123100 library-Soares fetal liver spleen lNFLS
           vector-pT73D (Pharmacia) with a modified polylinker host-DH10B
           (ampicillin resistant) primer--21m13 Rsite1-Pac I Rsite2-Eco RI
           Liver and spleen from a 20 week-post conception male fetus. 1st
           strand cDNA was primed with a Pac I - oligo(dT) primer [5',
           AACTGGAAGATTAATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded
           cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
           I and cloned into the Pac I and Eco RI sites of the modified pT73
           vector. Library went through one round of normalization. Library
           constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM    Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 496)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
           Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
           Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
           Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
           Wilson,R.
TITLE     The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
           WashU-Merck EST Project
           Washington University School of Medicine
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: est@watson.wustl.edu
           High quality sequence stops: 393
           Source: IMAGE Consortium, LLNL
           This clone is available royalty-free through LLNL; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES             source
BASE COUNT      116 a   126 c  125 g  126 t      3 others
ORIGIN

Query Match      100.0%; Score 9; DB 10; Length 436;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9
|||||
Db 334 TCTGAGTCA 342

RESULT 12
R00424
LOCUS      363 bp      mRNA      EST      31-MAR-1995
DEFINITION ye71h05.r1 Homo sapiens cDNA clone 123225 5'.
ACCESSION  R00424
NID         9750160
KEYWORDS   EST.
SOURCE     human clone-123225 library-Soares fetal liver spleen lNFLS
           vector-pT73D (Pharmacia) with a modified polylinker host-DH10B
           (ampicillin resistant) primer-M13RPI Rsite1-Pac I Rsite2-Eco RI
           Liver and spleen from a 20 week-post conception male fetus. 1st
           strand cDNA was primed with a Pac I - oligo(dT) primer [5',
           AACTGGAAGATTAATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded
           cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
           I and cloned into the Pac I and Eco RI sites of the modified pT73
           vector. Library went through one round of normalization. Library
           constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM    Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 363)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
           Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
           Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
           Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
           Wilson,R.
TITLE     The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   Contact: Wilson RK
           WashU-Merck EST Project
           Washington University School of Medicine
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: est@watson.wustl.edu
           High quality sequence stops: 202
           Source: IMAGE Consortium, LLNL
           This clone is available royalty-free through LLNL; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES             source
BASE COUNT      91 a   93 c   97 g   78 t      4 others
ORIGIN

Query Match      100.0%; Score 9; DB 10; Length 363;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9
|||||
Db 112 TCTGAGTCA 120

RESULT 13
R01268/c
LOCUS      411 bp      mRNA      EST      31-MAR-1995
DEFINITION ye81g05.s1 Homo sapiens cDNA clone 124184 3'.
ACCESSION  R01268
NID         9751004
KEYWORDS   EST.
SOURCE     human clone-124184 library-Soares fetal liver spleen lNFLS
           vector-pT73D (Pharmacia) with a modified polylinker host-DH10B
           (ampicillin resistant) primer--21m13 Rsite1-Pac I Rsite2-Eco RI
           Liver and spleen from a 20 week-post conception male fetus. 1st
           strand cDNA was primed with a Pac I - oligo(dT) primer [5',
           AACTGGAAGATTAATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded
           cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
           I and cloned into the Pac I and Eco RI sites of the modified pT73
           vector. Library went through one round of normalization. Library

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constructed by Bento Soares and M.Fatima Bonaído.  
Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 411)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
FEATURES  
source  
1..397  
/organism="Homo sapiens"  
/clone="123740"  
BASE COUNT 94 a 96 c 90 g 115 t 2 others  
ORIGIN  
Query Match 100.0%; Score 9; DB 10; Length 397;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 tctgagtca 9  
|||||  
Db 327 TCTGAGTCA 319  
RESULT 15  
R01864/c  
LOCUS R01864 379 bp mRNA EST 31-MAR-1995  
DEFINITION ye84d12.s1 Homo sapiens cDNA clone 124439 3'.  
ACCESSION R01864  
NID 9751600  
KEYWORDS  
SOURCE human clone=124439 library=Soares fetal liver spleen INFLS  
vector=PT73D (Pharmacia) with a modified polylinker host=DH10B  
(ampicillin resistant) primer=-21m13 Rsite1-Pac I Rsite2-Eco RI  
Liver and spleen from a 20 week-post conception male fetus. 1st  
strand cDNA was primed with a Pac I - oligo(dT) primer [5',  
AACGGAAGATTAATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac  
I and cloned into the Pac I and Eco RI sites of the modified pT73  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaído.  
ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 379)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 329  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
FEATURES  
source  
1..379  
/organism="Homo sapiens"  
/clone="124439"  
BASE COUNT 72 a 103 c 94 g 104 t 6 others  
ORIGIN

constructed by Bento Soares and M.Fatima Bonaído.  
Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 411)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 305  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
FEATURES  
source  
1..411  
/organism="Homo sapiens"  
/clone="124184"  
BASE COUNT 121 a 75 c 122 g 89 t 4 others  
ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 tctgagtca 9  
|||||  
Db 130 TCTGAGTCA 122  
RESULT 14  
R01396/c  
LOCUS R01396 397 bp mRNA EST 31-MAR-1995  
DEFINITION ye77a11.s1 Homo sapiens cDNA clone 123740 3' similar to contains  
Alu repetitive element.  
ACCESSION R01396  
NID 9751132  
KEYWORDS  
SOURCE human clone=123740 library=Soares fetal liver spleen INFLS  
vector=PT73D (Pharmacia) with a modified polylinker host=DH10B  
(ampicillin resistant) primer=-21m13 Rsite1-Pac I Rsite2-Eco RI  
Liver and spleen from a 20 week-post conception male fetus. 1st  
strand cDNA was primed with a Pac I - oligo(dT) primer [5',  
AACGGAAGATTAATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded  
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac  
I and cloned into the Pac I and Eco RI sites of the modified pT73  
vector. Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaído.  
ORGANISM Homo sapiens  
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 397)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
WashU-Merck EST Project

Query Match 100.0%; Score 9; DB 10; Length 379;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 tctgagtca 9  
| | | | | | | | | |  
Db 163 TCTGAGTCA 155

Search completed: June 23, 1999, 23:01:43  
Job time: 1627 sec

